

(19) World Intellectual Property Organization
International Bureau



(43) International Publication Date
18 October 2001 (18.10.2001)

PCT

(10) International Publication Number
WO 01/77372 A3

- (51) International Patent Classification⁷: **C12Q 1/68**
- (21) International Application Number: **PCT/BE01/00053**
- (22) International Filing Date: **26 March 2001 (26.03.2001)**
- (25) Filing Language: **English**
- (26) Publication Language: **English**
- (30) Priority Data:
00870055.1 24 March 2000 (24.03.2000) EP
00870204.5 15 September 2000 (15.09.2000) EP
- (71) Applicant (*for all designated States except US*): **FACULTES UNIVERSITAIRES NOTRE-DAME DE LA PAIX** [BE/BE]; Rue de Bruxelles 61, B-5000 Namur (BE).
- (72) Inventors; and
- (75) Inventors/Applicants (*for US only*): **REMACLE, José** [BE/BE]; Chemin des Pierres 4, B-5020 Malonne (BE). **HAMELS, Sandrine** [BE/BE]; Allée Saint Hubert 4, B-6280 Loverval (BE). **ZAMMATTEO, Nathalie** [BE/BE]; Avenue Jean Materne 202/3, B-5100 Jambes (BE). **LOCKMAN, Laurence** [BE/BE]; Rue Hemranlle 24, B-6600 Bastogne (BE). **DUFOUR, Sophie** [BE/BE]; Avenue du Quatrième Middlesex 22, B-7000 Mons (BE). **ALEXANDRE, Isabelle** [BE/BE]; Rue du Centre 3, B-5170 Lesve (BE). **DE LONGUEVILLE, Françoise** [BE/BE]; Avenue Jean Materne 110, B-5100 Jambes (BE).
- (74) Agents: **VAN MALDEREN, Eric et al.**; Office Van Malderen, Place Reine Fabiola 6/1, B-1083 Brussels (BE).
- (81) Designated States (*national*): AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW.
- (84) Designated States (*regional*): ARIPO patent (GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG).
- Published:**
— with international search report
— before the expiration of the time limit for amending the claims and to be republished in the event of receipt of amendments
- (88) Date of publication of the international search report:
13 June 2002
- For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.*

(54) Title: IDENTIFICATION OF BIOLOGICAL (MICRO) ORGANISMS BY DETECTION OF THEIR HOMOLOGOUS NUCLEOTIDE SEQUENCES ON ARRAYS

(57) Abstract: The present invention is related to an identification and/or quantification method of a biological (micro)organism or part of it by a detection of its nucleotide sequence among at least 4 other homologous sequences and comprising: amplifying or copying with a unique pair of primer(s), at least part of original nucleotide sequences (1) into target nucleotide sequences (2) to be detected; possibly labelling said target nucleotide sequences (2); putting into contact the labelled target nucleotide sequences (2) with single stranded capture nucleotide sequences (3) bound by a single predetermined link to an insoluble solid support (4), preferably a non porous solid support, discriminating the binding of a target nucleotide sequence (2) specific of an organism or part of it by detecting, quantifying and/or recording a signal resulting from a hybridization by complementary base pairing between the target nucleotide sequence (2) and its corresponding capture nucleotide sequence (3), wherein said capture nucleotide sequence (3) being bound to the insoluble solid support (4) at a determined location according to an array, said array having a density of at least 4 different bound single stranded capture nucleotide sequences/cm² of solid support surface.

INTERNATIONAL SEARCH REPORT

International Application No

PCT/BE 01/00053

A. CLASSIFICATION OF SUBJECT MATTER

IPC 7 C12Q1/68

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC 7 C12Q

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

EP0-Internal, WPI Data, BIOSIS, EMBASE, MEDLINE, CHEM ABS Data

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	WO 95 11995 A (AFFYMAX TECH NV ; FODOR STEPHEN P A (US); GINGERAS THOMAS R (US); L) 4 May 1995 (1995-05-04)	1-14,16, 24,25, 27,28
Y	the whole document	15,17, 26,29
X	WO 97 29212 A (GINGERAS THOMAS A ; CHEE MARK S (US); STRYER LUBERT (US); AFFYMETRI) 14 August 1997 (1997-08-14)	1-14,16, 24,25, 27,28
Y	the whole document	15,17, 26,29
X	WO 98 28444 A (UNIV CHICAGO) 2 July 1998 (1998-07-02)	1-14,16, 24,25, 27,28
Y	the whole document	15,17, 26,29
-/--		

☒ Further documents are listed in the continuation of box C.

☒ Patent family members are listed in annex.

* Special categories of cited documents :

"A" document defining the general state of the art which is not considered to be of particular relevance

"E" earlier document but published on or after the international filing date

"L" document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)

"O" document referring to an oral disclosure, use, exhibition or other means

"P" document published prior to the international filing date but later than the priority date claimed

"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.

"&" document member of the same patent family

Date of the actual completion of the international search

25 January 2002

Date of mailing of the international search report

10. 04. 2002

Name and mailing address of the ISA

European Patent Office, P.B. 5818 Patentlaan 2
NL - 2280 HV Rijswijk
Tel. (+31-70) 340-2040, Tx. 31 651 epo nl,
Fax: (+31-70) 340-3016

Authorized officer

Hagenmaier, S

INTERNATIONAL SEARCH REPORT

International Application No

PCT/BE 01/00053

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT		
Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	GUO Z ET AL: "DIRECT FLUORESCENCE ANALYSIS OF GENETIC POLYMORPHISMS BY HYBRIDIZATION WITH OLIGONUCLEOTIDE ARRAYS ON GLASS SUPPORTS" NUCLEIC ACIDS RESEARCH,GB,OXFORD UNIVERSITY PRESS, SURREY, vol. 22, no. 24, 11 December 1994 (1994-12-11), pages 5456-5465, XP002006248 ISSN: 0305-1048	1-14,16, 24,25
Y	the whole document	15,17, 26-29
Y	--- WO 99 16780 A (GALA JEAN LUC ;UNIV LOUVAIN (BE); MINISTERE DE LA DEFENSE NATION () 8 April 1999 (1999-04-08) the whole document	1-17, 24-29
Y	--- VANNUFFLE ET AL.: "Combined discrimination between Staphylococcus species and identification of methicillin resistance by a sandwich enzyme-linked oligo sorbent assay" ABSTRACTS OF THE INTERSCIENCE CONFERENCE ON ANTIMICROBIAL AGENTS AND CHEMOTHERAPY, vol. 39, 29 September 1999 (1999-09-29), page 208 XP001053081 the whole document	1-17, 24-29
Y	--- WO 89 11548 A (CETUS CORP) 30 November 1989 (1989-11-30) the whole document	1-17, 24-29
Y	--- EP 0 511 559 A (HOFFMANN LA ROCHE) 4 November 1992 (1992-11-04) the whole document	1-17, 24-29
Y	--- GB 2 318 791 A (ZENECA LTD) 6 May 1998 (1998-05-06) the whole document	1-17, 24-29
Y	--- US 5 683 872 A (TRUCCO MASSIMO ET AL) 4 November 1997 (1997-11-04) the whole document	1-17, 24-29
Y	--- VAN NESS J ET AL: "A VERSATILE SOLID SUPPORT SYSTEM FOR OLIGODEOXYNUCLEOTIDE PROBE-BASED HYBRIDIZATION ASSAYS" NUCLEIC ACIDS RESEARCH,GB,OXFORD UNIVERSITY PRESS, SURREY, vol. 19, no. 12, 25 June 1991 (1991-06-25), pages 3345-3350, XP000208399 ISSN: 0305-1048 the whole document	1-17, 24-29

	-/--	

INTERNATIONAL SEARCH REPORT

International Application No
PCT/BE 01/00053

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT		
Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	<p>WO 98 11253 A (ERNEST ISABELLE ;REMACLE JOSE (BE); ALEXANDRE ISABELLE (BE); ZAMMA) 19 March 1998 (1998-03-19) the whole document -----</p>	

INTERNATIONAL SEARCH REPORT

International application No.
PCT/BE 01/00053

Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:
2. ☐ Claims Nos.:
because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:
3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

see additional sheet

1. ☐ As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:
4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:
1-16, 24-28 (all partially), 17, 29 (completely)

Remark on Protest

- ☐ The additional search fees were accompanied by the applicant's protest.
- ☐ No protest accompanied the payment of additional search fees.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

This International Searching Authority found multiple (groups of) inventions in this international application, as follows:

1. Claims: 1-16, 24-28 (all partially), 17,29 (completely)

Diagnostic kit and method for the identification and/or quantification of a biological (micro) organism or part of it (possibly present in a biological sample) by a detection of its nucleotide sequence among at least 4 other homologous sequences and comprising the steps of :

-possibly extracting original nucleotide sequences (1) from the (micro) organism ;

-amplifying or copying with a unique pair of primer(s), at least part of original nucleotide sequences (1) into target nucleotide sequences (2) to be detected ;

-possibly labelling said target nucleotide sequences (2) ;

-putting into contact the labelled target nucleotide sequences (2) with single stranded capture nucleotide sequences (3) bound by a single predetermined link to an insoluble solid support (4), preferably a non porous solid support,

-discriminating the binding of a target nucleotide sequence (2) specific of an organism or part of it by detecting, quantifying and/or recording a signal resulting from a hybridization by complementary base pairing between the target nucleotide sequence (2) and its corresponding capture nucleotide sequence (3), wherein said capture nucleotide sequence (3) being bound to the insoluble solid support (4) at a determined location according to an array, said array having a density of at least 4 different bound single stranded capture nucleotide sequences/cm² of solid support surface and wherein the binding between the target nucleotide sequence and its corresponding capture nucleotide sequence forms (will result in) said signal at determined location, the detection of a single signal allowing a discrimination and identification of the target nucleotide sequence specific of an organism or part of it from homologous nucleotide sequences wherein the solid support bears capture nucleotide sequences specific for the identification of two or more Staphylococcus species together with a consensus sequence for a Staphylococcus genus identification.

2. Claims: 1-16, 24-28 (all partially), 18,30 (completely)

Diagnostic kit and method for the identification and/or quantification of a biological (micro) organism or part of it (possibly present in a biological sample) by a detection of its nucleotide sequence among at least 4 other homologous sequences and comprising the steps of :

-possibly extracting original nucleotide sequences (1) from the (micro) organism ;

-amplifying or copying with a unique pair of primer(s), at least part of original nucleotide sequences (1) into target

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

nucleotide sequences (2) to be detected ;

- possibly labelling said target nucleotide sequences (2) ;
- putting into contact the labelled target nucleotide sequences (2) with single stranded capture nucleotide sequences (3) bound by a single predetermined link to an insoluble solid support (4), preferably a non porous solid support,
- discriminating the binding of a target nucleotide sequence (2) specific of an organism or part of it by detecting, quantifying and/or recording a signal resulting from a hybridization by complementary base pairing between the target nucleotide sequence (2) and its corresponding capture nucleotide sequence (3), wherein said capture nucleotide sequence (3) being bound to the insoluble solid support (4) at a determined location according to an array, said array having a density of at least 4 different bound single stranded capture nucleotide sequences/cm² of solid support surface and wherein the binding between the target nucleotide sequence and its corresponding capture nucleotide sequence forms (will result in) said signal at determined location, the detection of a single signal allowing a discrimination and identification of the target nucleotide sequence specific of an organism or part of it from homologous nucleotide sequences wherein the original sequence to be identified and/or quantified in the sample belongs to the MAGE gene family.

3. Claims: 1-16, 24-28 (all partially), 19,31 (completely)

Diagnostic kit and method for the identification and/or quantification of a biological (micro) organism or part of it (possibly present in a biological sample) by a detection of its nucleotide sequence among at least 4 other homologous sequences and comprising the steps of :

- possibly extracting original nucleotide sequences (1) from the (micro) organism ;
- amplifying or copying with a unique pair of primer(s), at least part of original nucleotide sequences (1) into target nucleotide sequences (2) to be detected ;
- possibly labelling said target nucleotide sequences (2) ;
- putting into contact the labelled target nucleotide sequences (2) with single stranded capture nucleotide sequences (3) bound by a single predetermined link to an insoluble solid support (4), preferably a non porous solid support,
- discriminating the binding of a target nucleotide sequence (2) specific of an organism or part of it by detecting, quantifying and/or recording a signal resulting from a hybridization by complementary base pairing between the target nucleotide sequence (2) and its corresponding capture nucleotide sequence (3), wherein said capture nucleotide sequence (3) being bound to the insoluble solid support (4) at a determined location according to an array, said array having a density of at least 4 different bound single

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

stranded capture nucleotide sequences/cm² of solid support surface and wherein the binding between the target nucleotide sequence and its corresponding capture nucleotide sequence forms (will result in) said signal at determined location, the detection of a single signal allowing a discrimination and identification of the target nucleotide sequence specific of an organism or part of it from homologous nucleotide sequences wherein the original sequence to be identified and/or quantified in the sample belongs to the HLA-A genes family.

4. Claims: 1-16, 24-28,32 (all partially), 20,33 (completely)

Diagnostic kit and method for the identification and/or quantification of a biological (micro) organism or part of it (possibly present in a biological sample) by a detection of its nucleotide sequence among at least 4 other homologous sequences and comprising the steps of :

- possibly extracting original nucleotide sequences (1) from the (micro) organism ;
- amplifying or copying with a unique pair of primer(s), at least part of original nucleotide sequences (1) into target nucleotide sequences (2) to be detected ;
- possibly labelling said target nucleotide sequences (2) ;
- putting into contact the labelled target nucleotide sequences (2) with single stranded capture nucleotide sequences (3) bound by a single predetermined link to an insoluble solid support (4), preferably a non porous solid support,
- discriminating the binding of a target nucleotide sequence (2) specific of an organism or part of it by detecting, quantifying and/or recording a signal resulting from a hybridization by complementary base pairing between the target nucleotide sequence (2) and its corresponding capture nucleotide sequence (3), wherein said capture nucleotide sequence (3) being bound to the insoluble solid support (4) at a determined location according to an array, said array having a density of at least 4 different bound single stranded capture nucleotide sequences/cm² of solid support surface and wherein the binding between the target nucleotide sequence and its corresponding capture nucleotide sequence forms (will result in) said signal at determined location, the detection of a single signal allowing a discrimination and identification of the target nucleotide sequence specific of an organism or part of it from homologous nucleotide sequences wherein the original sequence to be identified and/or quantified in the sample belongs to the dopamine receptors coupled to the protein G genes family.

5. Claims: 1-16, 24-28 (all partially), 21 (completely)

Diagnostic kit and method for the identification and/or

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

quantification of a biological (micro) organism or part of it (possibly present in a biological sample) by a detection of its nucleotide sequence among at least 4 other homologous sequences and comprising the steps of :

- possibly extracting original nucleotide sequences (1) from the (micro) organism ;
- amplifying or copying with a unique pair of primer(s), at least part of original nucleotide sequences (1) into target nucleotide sequences (2) to be detected ;

- possibly labelling said target nucleotide sequences (2) ;

- putting into contact the labelled target nucleotide sequences (2) with single stranded capture nucleotide sequences (3) bound by a single predetermined link to an insoluble solid support (4), preferably a non porous solid support,

- discriminating the binding of a target nucleotide sequence (2) specific of an organism or part of it by detecting, quantifying and/or recording a signal resulting from a hybridization by complementary base pairing between the target nucleotide sequence (2) and its corresponding capture nucleotide sequence (3), wherein said capture nucleotide sequence (3) being bound to the insoluble solid support (4) at a determined location according to an array, said array having a density of at least 4 different bound single stranded capture nucleotide sequences/cm² of solid support surface and wherein the binding between the target nucleotide sequence and its corresponding capture nucleotide sequence forms (will result in) said signal at determined location, the detection of a single signal allowing a discrimination and identification of the target nucleotide sequence specific of an organism or part of it from homologous nucleotide sequences wherein the original sequence to be identified and/or quantified in the sample belongs to the choline receptors coupled to the protein G genes family.

6. Claims: 1-16, 24-28,32 (all partially),22,35 (completely)

Diagnostic kit and method for the identification and/or quantification of a biological (micro) organism or part of it (possibly present in a biological sample) by a detection of its nucleotide sequence among at least 4 other homologous sequences and comprising the steps of :

- possibly extracting original nucleotide sequences (1) from the (micro) organism ;

- amplifying or copying with a unique pair of primer(s), at least part of original nucleotide sequences (1) into target nucleotide sequences (2) to be detected ;

- possibly labelling said target nucleotide sequences (2) ;

- putting into contact the labelled target nucleotide sequences (2) with single stranded capture nucleotide sequences (3) bound by a single predetermined link to an insoluble solid support (4), preferably a non porous solid support,

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

-discriminating the binding of a target nucleotide sequence (2) specific of an organism or part of it by detecting, quantifying and/or recording a signal resulting from a hybridization by complementary base pairing between the target nucleotide sequence (2) and its corresponding capture nucleotide sequence (3), wherein said capture nucleotide sequence (3) being bound to the insoluble solid support (4) at a determined location according to an array, said array having a density of at least 4 different bound single stranded capture nucleotide sequences/cm² of solid support surface and wherein the binding between the target nucleotide sequence and its corresponding capture nucleotide sequence forms (will result in) said signal at determined location, the detection of a single signal allowing a discrimination and identification of the target nucleotide sequence specific of an organism or part of it from homologous nucleotide sequences wherein the original sequence to be identified and/or quantified in the sample belongs to the histamine receptors coupled to the protein G genes family.

7. Claims: 1-16, 24-28 (all partially), 23,37 (completely)

Diagnostic kit and method for the identification and/or quantification of a biological (micro) organism or part of it (possibly present in a biological sample) by a detection of its nucleotide sequence among at least 4 other homologous sequences and comprising the steps of :

- possibly extracting original nucleotide sequences (1) from the (micro) organism ;
- amplifying or copying with a unique pair of primer(s), at least part of original nucleotide sequences (1) into target nucleotide sequences (2) to be detected ;
- possibly labelling said target nucleotide sequences (2) ;
- putting into contact the labelled target nucleotide sequences (2) with single stranded capture nucleotide sequences (3) bound by a single predetermined link to an insoluble solid support (4), preferably a non porous solid support,
- discriminating the binding of a target nucleotide sequence (2) specific of an organism or part of it by detecting, quantifying and/or recording a signal resulting from a hybridization by complementary base pairing between the target nucleotide sequence (2) and its corresponding capture nucleotide sequence (3), wherein said capture nucleotide sequence (3) being bound to the insoluble solid support (4) at a determined location according to an array, said array having a density of at least 4 different bound single stranded capture nucleotide sequences/cm² of solid support surface and wherein the binding between the target nucleotide sequence and its corresponding capture nucleotide sequence forms (will result in) said signal at determined location, the detection of a single signal allowing a discrimination and identification of the target nucleotide

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

sequence specific of an organism or part of it from homologous nucleotide sequences wherein the original sequence to be identified and/or quantified in the sample belongs to the cytochrome P450 forms family.

8. Claims: 24-25,27,28,32 (all partially), 34 (completely)

Diagnostic kit for performing a method for identification and/or quantification of a biological (micro) organism or part of it (possibly present in a biological sample) by a detection of its nucleotide sequence among at least 4 other homologous sequences and comprising the steps of :

- possibly extracting original nucleotide sequences (1) from the (micro) organism ;
- amplifying or copying with a unique pair of primer(s), at least part of original nucleotide sequences (1) into target nucleotide sequences (2) to be detected ;
- possibly labelling said target nucleotide sequences (2) ;
- putting into contact the labelled target nucleotide sequences (2) with single stranded capture nucleotide sequences (3) bound by a single predetermined link to an insoluble solid support (4), preferably a non porous solid support,
- discriminating the binding of a target nucleotide sequence (2) specific of an organism or part of it by detecting, quantifying and/or recording a signal resulting from a hybridization by complementary base pairing between the target nucleotide sequence (2) and its corresponding capture nucleotide sequence (3), wherein said capture nucleotide sequence (3) being bound to the insoluble solid support (4) at a determined location according to an array, said array having a density of at least 4 different bound single stranded capture nucleotide sequences/cm² of solid support surface and wherein the binding between the target nucleotide sequence and its corresponding capture nucleotide sequence forms (will result in) said signal at determined location, the detection of a single signal allowing a discrimination and identification of the target nucleotide sequence specific of an organism or part of it from homologous nucleotide sequences wherein the original sequence to be identified and/or quantified in the sample belongs to the serotonin receptors coupled to the protein G genes family.

9. Claims: 24-28 (all partially), 36 (completely)

Diagnostic kit for performing a method for identification and/or quantification of a biological (micro) organism or part of it (possibly present in a biological sample) by a detection of its nucleotide sequence among at least 4 other homologous sequences and comprising the steps of :

- possibly extracting original nucleotide sequences (1) from the (micro) organism ;

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

-amplifying or copying with a unique pair of primer(s), at least part of original nucleotide sequences (1) into target nucleotide sequences (2) to be detected ;
-possibly labelling said target nucleotide sequences (2) ;
-putting into contact the labelled target nucleotide sequences (2) with single stranded capture nucleotide sequences (3) bound by a single predetermined link to an insoluble solid support (4), preferably a non porous solid support,
-discriminating the binding of a target nucleotide sequence (2) specific of an organism or part of it by detecting, quantifying and/or recording a signal resulting from a hybridization by complementary base pairing between the target nucleotide sequence (2) and its corresponding capture nucleotide sequence (3), wherein said capture nucleotide sequence (3) being bound to the insoluble solid support (4) at a determined location according to an array, said array having a density of at least 4 different bound single stranded capture nucleotide sequences/cm² of solid support surface and wherein the binding between the target nucleotide sequence and its corresponding capture nucleotide sequence forms (will result in) said signal at determined location, the detection of a single signal allowing a discrimination and identification of the target nucleotide sequence specific of an organism or part of it from homologous nucleotide sequences wherein the sequence to be identified and/or quantified in the sample are gene sequences of GMO plants.

INTERNATIONAL SEARCH REPORT

Information on patent family members

International Application No

PCT/BE 01/00053

Patent document cited in search report		Publication date	Patent family member(s)	Publication date
WO 9511995	A	04-05-1995	AU 8126694 A EP 0730663 A1 JP 9507121 T WO 9511995 A1 US 6156501 A US 6045996 A US 6309823 B1 US 5861242 A US 5837832 A	22-05-1995 11-09-1996 22-07-1997 04-05-1995 05-12-2000 04-04-2000 30-10-2001 19-01-1999 17-11-1998
WO 9729212	A	14-08-1997	AU 2189397 A EP 0937159 A1 JP 2000504575 T WO 9729212 A1 US 6228575 B1	28-08-1997 25-08-1999 18-04-2000 14-08-1997 08-05-2001
WO 9828444	A	02-07-1998	AU 5716098 A EP 0951569 A2 WO 9828444 A2	17-07-1998 27-10-1999 02-07-1998
WO 9916780	A	08-04-1999	WO 9916780 A2 CA 2301285 A1 EP 1017850 A2 JP 2001518283 T	08-04-1999 08-04-1999 12-07-2000 16-10-2001
WO 8911548	A	30-11-1989	AT 173508 T AU 632494 B2 AU 3754289 A DE 68928853 D1 DE 68928853 T2 EP 0451141 A1 IE 164389 L IL 90358 A JP 2897959 B2 JP 3504328 T WO 8911548 A1	15-12-1998 07-01-1993 12-12-1989 24-12-1998 05-08-1999 16-10-1991 20-11-1989 18-08-1993 31-05-1999 26-09-1991 30-11-1989
EP 0511559	A	04-11-1992	AU 1506292 A BR 9201591 A CA 2067426 A1 EP 0511559 A1 JP 5168499 A NO 921683 A NZ 242508 A ZA 9202950 A	05-11-1992 01-12-1992 31-10-1992 04-11-1992 02-07-1993 02-11-1992 26-07-1994 20-09-1993
GB 2318791	A	06-05-1998	EP 0935671 A1 WO 9818961 A1 JP 2001502909 T	18-08-1999 07-05-1998 06-03-2001
US 5683872	A	04-11-1997	EP 0656065 A1 JP 7500734 T WO 9309245 A1	07-06-1995 26-01-1995 13-05-1993
WO 9811253	A	19-03-1998	BE 1010608 A3 BE 1011052 A3 WO 9811253 A2 EP 0929696 A2	03-11-1998 06-04-1999 19-03-1998 21-07-1999

INTERNATIONAL SEARCH REPORT

Information on patent family members

International Application No

PCT/BE 01/00053

Patent document cited in search report	Publication date	Patent family member(s)	Publication date
WO 9811253	A	US 2001010906 A1	02-08-2001
